Shouryan Patil

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Motivated M.Sc. Bioinformatics graduate skilled in computational biology, transcriptomics, and drug discovery. I'm proficient in Python, R, RNA-Seq analysis, and molecular docking, with experience in cancer drug repurposing and gene expression projects. After a 6-month internship, I'm eager to join a research team, contribute to meaningful discoveries, and prepare for a Ph.D. abroad.

WORK EXPERIENCE

BVG Life Sciences Limited   **Chinchwad, Pune**
Computational biology and R&D Intern   *April 2024 – October 2024*
- **Advanced Molecular Docking:** Used AutoDock4 and AutoDock Vina to identify herbal ligands for disease-targeted proteins, aiding novel drug discovery.
- **Data Visualization & Analysis:** Leveraged R for docking result visualization and molecular interaction analysis, ensuring precise reporting.

CODSOFT   **Remote**
Python Programming Intern   *February 2024 – February 2024*
- **Python Development Projects:** Built a To-Do List app, calculator, password generator, and Rock-Paper-Scissors game, showcasing problem-solving and programming skills.
- **GUI & Logic Implementation:** Developed interactive applications with user-friendly interfaces and functional logic using Python.

EDUCATION

M.Sc. Bioinformatics *(CGPA: 8.31)*   **Pimpri, Pune**
Dr. D. Y. Patil Arts, Commerce & Science College   *June 2023 – April 2025*
B.Sc. Biotechnology *(CGPA: 8.00)*   **Ganeshkhind, Pune**
Modern College of Arts, Science & Commerce   *June 2020 – April 2023*
Senior Secondary Education (12th Grade) *(60%)*   **Kasba Peth, Pune**
Acharya Shri D. B. Dadawala Junior College   *June 2019 – April 2020*
Matric (10th Grade) *(72.20%)*   **Shivajinagar, Pune**
Modern High School   *June 2017 – April 2018*

SKILLS

Programming & Scripting: Python (Biopython, pandas) | R (ggplot2, DEXSeq) | Bash | Linux
Transcriptomics & RNA-seq: HISAT2 | Samtools | Bedtools | Leafcutter | Bioconductor (DESeq2, edgeR) | RNA-seq Analysis
Bioinformatics Tools: AutoDock | GROMACS | UCSC Genome Browser | MySQL
Visualization & Analysis: Matplotlib | seaborn | ggplot2
Other Tools: Git | GitHub | MS Excel | Power BI

PROJECT

RNA-Seq Analysis for CAR-T Target Discovery *([Link](#))*   **March, 2025**
Performed RNA-Seq analysis using TCGA breast cancer data to identify upregulated surface-expressed genes as potential CAR-T cell therapy targets. Used DESeq2 in R to analyze tumor vs. normal samples and identified 28 significantly overexpressed genes, including KIAA0319, CA9, and CEACAM6. Generated PCA, MA, volcano, heatmap, and boxplot visualizations to support findings.

Drug Repurposing for Colorectal Cancer *([Link](#))*   **November, 2024 - February, 2025**
Conducted an in-silico drug repurposing study for colorectal cancer, targeting key oncogenic pathways (EGFR/MAPK, Wnt/β-catenin, and PI3K/AKT). Utilized molecular docking and molecular dynamics simulations to screen FDA-approved drugs. Identified Pazopanib and Brequinar as promising candidates with strong binding affinities and favorable pharmacokinetic profiles.

Automated Docking Pipeline with AutoDock Vina *([Link](#))*   **January, 2025**
Developed a Python-based automation script for molecular docking with AutoDock Vina, enabling large-scale ligand screening. Automated docking, extracted binding affinities, and ranked ligands to accelerate drug discovery.

CERTIFICATIONS

Certifications: Genetics and NGS for Bioinformatics (Udemy) | Linux Tutorial (Great Learning) | My SQL Basics (Great Learning) | Business Intelligence using Power BI (Skill Nation) | R Programming Language (Great Learning) | Excel for Beginners (Great Learning)